



16988 ST25.txt

SEQUENCE LISTING

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Prince, Alfred M.

<120> METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS

<130> 323-100USD

<140> 10/677,956

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<150> 08/931,855

<151> 1997-09-16

<150> 08/563,733

<151> 1995-11-08

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<150> 07/573,643

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<160> 76

<170> PatentIn version 3.3

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His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
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gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147

Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243

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Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
 65 70 75
 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291
 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
 80 85 90
 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act 339
 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
 95 100 105
 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct 387
 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
 110 115 120
 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat 435
 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
 125 130 135 140
 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa 483
 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
 145 150 155
 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act 531
 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
 160 165 170
 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa 579
 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
 175 180 185
 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa 627
 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
 190 195 200
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 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
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 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt 723
 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys
 225 230 235
 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc 771
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 His Lys Ala Arg Val Leu
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 <213> Human immunodeficiency virus

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Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
210 215 220

Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
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Val Leu

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 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
 15 20 25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147
 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
 30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195
 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
 45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243
 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
 65 70 75

gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291
 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
 80 85 90

gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act 339
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 95 100 105

act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct 387
 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
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atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat 435
 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
 125 130 135 140

aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa 483
 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
 145 150 155

gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act 531
 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
 160 165 170

cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa 579
 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
 175 180 185

acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa 627
 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
 190 195 200

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gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag	675
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Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys	
225 230 235	
aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc	771
Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly	
240 245 250	
cat aag gca aga gtt ttg taataa	795
His Lys Ala Arg Val Leu	
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Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala	
35 40 45	
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
50 55 60	
Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu	
65 70 75 80	
Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln	
85 90 95	
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu	
100 105 110	
Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly	
115 120 125	
Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg	
130 135 140	
Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu	
145 150 155 160	

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Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
210 215 220

Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu
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Val Leu

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His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
15 20 25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147
Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243
Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
65 70 75

gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291
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Ala Pro Gly Gln Met Arg Glu Pro 100	Arg Gly Ser Asp Ile 105	Ala Gly Thr	
act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct			387
Thr Ser 110 Thr Leu Gln Glu Gln Ile 115	Thr Asn 120	Asn Pro Pro	
atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat			435
Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile 135	Ile Leu Gly Leu Asn 140		
aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa			483
Lys Ile Val Arg Met 145 Tyr Ser Pro Thr 150	Ile Asp Ile Arg Gln 155		
gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act			531
Gly Pro Lys Glu Pro Phe Arg Asp Tyr 165	Val Asp Arg Phe Tyr 170	Lys Thr	
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Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu			
acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa			627
Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr 200	Ile Leu Lys		
gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag			675
Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln			
205 210 215 220			
gga gta gga gga cca caa aat caa caa ctt tta aat tta tgg ggg tgt			723
Gly Val Gly Gly Pro Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys			
225 230 235			
aga ggg aaa gct att tgt tat act tcc gtt caa tgg aat gga ccc ggc			771
Arg Gly Lys Ala Ile Cys Tyr Thr Ser Val Gln Trp Asn Gly Pro Gly			
240 245 250			
cat aag gca aga gtt ttg taataa			795
His Lys Ala Arg Val Leu			
255			

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Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
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35

40

45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
 50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
 65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
 85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
 100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
 115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
 130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
 145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
 165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
 180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
 195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
 210 215 220

Pro Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Arg Gly Lys Ala
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 Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
 30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195
 Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
 45 50 55 60

aga cgt cag cct atc ccc aag gtg cgt cgg ccg gag ggc agg acc tgg 243
 Arg Arg Gln Pro Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp
 65 70 75

gct cag ccc ggg tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg 291
 Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
 80 85 90

tgg gcg gga tgg ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339
 Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
 95 100 105

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 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

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Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
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Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
45 50 55 60

aga cgt cag cct atc ccc aag gca cgt cgg ccc gag ggc agg acc tgg 243
Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp
65 70 75

gct cag ccc ggg tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg 291
Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
80 85 90

tgg gcg gga tgg ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
95 100 105

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Pro Thr Asp Pro Arg Arg Ser Arg Asn Leu Gly
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35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
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Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
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Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
30 35 40

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Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
45 50 55 60

16988 ST25.txt

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Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp
65 70 75

ggt aag ccc ggg tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg 291
Gly Lys Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
80 85 90

tgg gcg gga tgg ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
95 100 105

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<210> 12
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20 25 30

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35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
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100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly
115 120

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<222> (16)..(375)

<400> 13

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                        1                5                10

cgt aac acc aac cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt      99
Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                        15                20                25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg      147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
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Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
45                50                55                60

aga cgt cag cct atc ccc aag gca cgt cgg tcc gag ggc agg tcc tgg      243
Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp
                        65                70                75

gct cag ccc ggg tac cct tgg ccc ctg tat ggc aat gag ggt tgc ggg      291
Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
                        80                85                90

tgg gcg gga tgg ctg ctg tct ccc cgt ggc tct cgg cct agc tgg ggc      339
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
                        95                100                105

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Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly
110                115                120

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<210> 14

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<213> Hepatitis C virus

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Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35                40                45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50                55                60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                70                75                80

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16988 ST25.txt

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
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Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly
115 120

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Met Pro Ile His His His His His His His Gly Pro Gly
1 5 10

tcc gtc act gtg tcc cat cct aac atc gag gag gtt gct ctg tcc acc 99
Ser Val Thr Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
15 20 25

acc gga gag atc ccc ttt tac ggc aag gct atc ccc ctc gag gtg atc 147
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
30 35 40

aag ggg gga aga cat ctc atc ttc tgc cac tca aag aag aag tgc gac 195
Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
45 50 55 60

gag ctc gcc gcg aag ctg gtc gca ttg ggc atc aat gcc gtg gcc tac 243
Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr
65 70 75

tac cgc ggt ctt gac gtg tct gtc atc ccg acc agc ggc gat gtt gtc 291
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
80 85 90

gtc gtg tca acc gat gct ctc atg act ggc ttt acc ggc gac ttc gac 339
Val Val Ser Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp
95 100 105

tcg gtg ata gac tgc aat acg ggt acc gag ctc gaa ttc taa 381
Ser Val Ile Asp Cys Asn Thr Gly Thr Glu Leu Glu Phe
110 115 120

<210> 16
<211> 121
<212> PRT
<213> Hepatitis C virus

<400> 16

16988 ST25.txt

Met Pro Ile His His His His His His Gly Pro Gly Ser Val Thr Val
 1 5 10 15

Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile
 20 25 30

Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg
 35 40 45

His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala
 50 55 60

Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu
 65 70 75 80

Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ser Thr
 85 90 95

Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp
 100 105 110

Cys Asn Thr Gly Thr Glu Leu Glu Phe
 115 120

<210> 17
 <211> 774
 <212> DNA
 <213> Hepatitis C virus

<220>
 <221> CDS
 <222> (16)..(771)

<400> 17
 aggaggggttt ttcat atg tcc cct ata cta ggt tat tgg aaa att aag ggc 51
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
 1 5 10

ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat 99
 Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
 15 20 25

gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa 147
 Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
 30 35 40

aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat 195
 Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
 45 50 55 60

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct 243
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
 65 70 75

16988 ST25.txt

gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca gag att 291
 Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile
 80 85 90
 tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt gtt tcg aga 339
 Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
 95 100 105
 att gca tat agt aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc 387
 Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
 110 115 120
 aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa 435
 Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys
 125 130 135 140
 aca tat tta aat ggt gat cat gta acc cat cct gac ttc atg ttg tat 483
 Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
 145 150 155
 gac gct ctt gat gtt gtt tta tac atg gac cca atg tgc ctg gat gcg 531
 Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
 160 165 170
 ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa 579
 Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
 175 180 185
 att gat aag tac ttg aaa tcc agc aag tat ata gca tgg cct ttg cag 627
 Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
 190 195 200
 ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat 675
 Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp
 205 210 215 220
 ctg gtt ccg cgt gga tcc gac gtc aag ttc ccg ggt ggc ggt cag atc 723
 Leu Val Pro Arg Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
 225 230 235
 gtt ggt gga gtt tac ttg ttg ccg cgc agg gaa ttc atc gtg act gac 771
 Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
 240 245 250
 tga 774

<210> 18
 <211> 252
 <212> PRT
 <213> Hepatitis C virus

<400> 18

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val
 225 230 235 240

Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
 245 250

<210> 19
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 19
ccaaaattac catatgccaa tcgtgcagaa c 31

<210> 20
<211> 33
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 20
gacccggcca taaggcaaga gttttgtaat aag 33

<210> 21
<211> 34
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 21
gatccttatt acaaaaactct tgccttatgg ccgg 34

<210> 22
<211> 28
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 22
gctcgcatat gagcacgatt cccaaacc 28

<210> 23
<211> 32
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 23
gacgaattct taaccCAAat tgcgcgacct ac 32

<210> 24
<211> 66
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 24
gatccgacgt caagttcccg ggtggcggtc agatcggttg tggagtttac ttgttgccgc 60

gcaggg 66

<210> 25
 <211> 66
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 25
 aattccctgc gcggcaacaa gtaaactcca ccaacgatct gaccgccacc cggggaacttg 60
 acgtcg 66

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 26
 ggaattccat atgtccccta tactaggt 28

<210> 27
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 27
 cggaattctc acctgcgcgg caacaa 26

<210> 28
 <211> 52
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 28
 tatgcctatt catcatcatc atcatcatgg cccgggaatt ctaagtaagt ag 52

<210> 29
 <211> 54
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 29

gatcctactt acttagaatt cccgggccat gatgatgatg atgatgaata ggca

54

<210> 30
 <211> 978
 <212> DNA
 <213> non-A, non-B hepatitis virus

<220>
 <221> CDS
 <222> (1)..(978)
 <223> non-A, non-B hepatitis virus structural antigen

<400> 30
 atg agc acg att ccc aaa cgt caa aga aaa acc aaa cgt aac acc aac 48
 Met Ser Thr Ile Pro Lys Arg Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt 96
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg 144
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45

acg agg aag act tcc gag cgg tcg caa cct cga ggt aga cgt cag cct 192
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

atc ccc aag gca cgt cgg ccc gag ggc agg acc tgg gct cag ccc ggg 240
 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
 65 70 75 80

tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg 288
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95

ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc ccc aca gac ccc 336
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110

cgg cgt agg tcg cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc 384
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

ggc ttc gcc gac ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt 432
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
 130 135 140

gga ggc gct gcc agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac 480
 Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

ggc gtg aac tat gca aca ggg aac ctt cct ggt tgc tct ttc tct atc 528
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

ttc ctt ctg gcc ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac 576
 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr
 180 185 190

16988 ST25.txt

caa gtg cgc aat tcc tcg ggg ctt tac cat gtc acc aat gat tgc cct	624
Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp Cys Pro	
195 200 205	
aac tcg agt gtt gtg tac gag gcg gcc gat gcc atc ctg cac act ccg	672
Asn Ser Ser Val Val Tyr Glu Ala Ala Asp Ala Ile Leu His Thr Pro	
210 215 220	
ggg tgt gtc cct tgc gtt cgc gag ggt aac gcc tcg agg tgt tgg gtg	720
Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser Arg Cys Trp Val	
225 230 235 240	
gcg gtg acc ccc acg gtg gcc acc agg gac ggc aaa ctt ccc aca acg	768
Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr	
245 250 255	
cag ctt cga cgt cat atc gat ctg ctt gtc ggg agc gcc acc ctc tgc	816
Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala Thr Leu Cys	
260 265 270	
tcg gcc ctc tac gtg ggg gac ctg tgc ggg tct gtc ttt ctc gtt ggt	864
Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Gly	
275 280 285	
caa ctg ttt acc ttc tct ccc agg cgc cac tgg acg acg caa gac tgc	912
Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Asp Cys	
290 295 300	
aat tgt tct atc tat ccc ggc cat ata acg ggt cat cgc atg gca tgg	960
Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp	
305 310 315 320	
gat atg atg atg aac tgg	978
Asp Met Met Met Asn Trp	
325	

<210> 31
 <211> 948
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a fusion protein that includes sequences from
 glutathione-S-transferase, non-A, non-B hepatitis virus capsid
 antigen, and a Factor X cleavage site

<220>
 <221> CDS
 <222> (1)..(945)

<400> 31	
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	

16988 ST25.txt

ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	ggt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
gga	gcg	ggt	ttg	gat	att	aga	tac	ggt	ggt	tcg	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
aaa	gac	ttt	gaa	act	ctc	aaa	ggt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
ggt	ggt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
ggt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	atc	gaa	ggt	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Ile	Glu	Gly	
	210					215					220					
cgt	ggg	atc	ccc	aat	tcg	agc	tcg	gta	ccc	atg	agc	acg	att	ccc	aaa	720
Arg	Gly	Ile	Pro	Asn	Ser	Ser	Ser	Val	Pro	Met	Ser	Thr	Ile	Pro	Lys	
	225				230					235					240	
cct	caa	aga	aaa	acc	aaa	cgt	aac	acc	aac	cgt	cgc	cca	cag	gac	gtc	768
Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	
				245					250					255		
aag	ttc	ccg	ggt	ggc	ggt	cag	atc	ggt	ggt	gga	ggt	tac	ttg	ttg	ccg	816
Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	
			260					265					270			
cgc	agg	ggc	cct	aga	ttg	ggt	gtg	cgc	gcg	acg	agg	aag	act	tcc	gag	864
Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	
		275					280					285				
cgg	tcg	caa	cct	cga	ggt	aga	cgt	cag	cct	atc	ccc	aag	gca	cgt	cgg	912
Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg	

290

295

ccc gag ggc agg acg ggg atc ggg aat tca tcg tga
Pro Glu Gly Arg Thr Gly Ile Gly Asn Ser Ser
305 310 315

948

<210> 32
<211> 21
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 32
atgagcacga ttcccaaacc t

21

<210> 33
<211> 17
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 33
gaggaagact tccgagc

17

<210> 34
<211> 17
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 34
gtcctgccct cgggccg

17

<210> 35
<211> 21
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 35
acccaaattg cgcgacctac g

21

<210> 36
<211> 19
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 36
 tgggtaaggc catcgatac 19

<210> 37
 <211> 17
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 37
 aaggtcatcg ataccct 17

<210> 38
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 38
 agatagagaa agagcaac 18

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 39
 ggaccagttc atcatcatat at 22

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 40
 cagttcatca tcatatccca 20

<210> 41
 <211> 5
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 41

Gly Ile Pro Asn Ser
1 5

<210> 42
<211> 15
<212> DNA
<213> Artificial

<220>
<223> Codes for linker protein in GST-NANBV 693-691

<220>
<221> CDS
<222> (1)..(15)

<400> 42
ggg atc ccc aat tca
Gly Ile Pro Asn Ser
1 5

15

<210> 43
<211> 3
<212> PRT
<213> Artificial

<220>
<223> Carboxy-terminal linker protein in GST-NANBV 693-691

<400> 43

Asn Ser Ser
1

<210> 44
<211> 12
<212> DNA
<213> Artificial

<220>
<223> Codes for carboxy-terminal linker protein in GST-NANBV 693-691

<220>
<221> CDS
<222> (1)..(9)

<400> 44
aat tca tcg tga
Asn Ser Ser
1

12

<210> 45
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Linker protein in GST-NANBV 15-18

<400> 45

Gly Ile Pro Ile Glu Phe Leu Gln Pro
 1 5

<210> 46

<211> 27

<212> DNA

<213> Artificial

<220>

<221> CDS

<222> (1)..(27)

<223> Codes for linker protein in GST-NANBV 15-18

<400> 46

ggg atc ccc atc gaa ttc ctg cag ccc
 Gly Ile Pro Ile Glu Phe Leu Gln Pro
 1 5

27

<210> 47

<211> 7

<212> PRT

<213> Artificial

<220>

<223> Carboxy-terminal linker protein in GST-NANBV 15-18

<400> 47

Trp Gly Ile Gly Asn Ser Ser
 1 5

<210> 48

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Codes for carboxy-terminal linker protein in GST-NANBV 15-18

<220>

<221> CDS

<222> (1)..(21)

<400> 48

tgg ggg atc ggg aat tca tcg tga
 Trp Gly Ile Gly Asn Ser Ser
 1 5

24

<210> 49

<211> 8

<212> PRT

<213> Artificial

<220>

<223> Linker protein in GST-NANBV 15-17

<400> 49

Gly Ile Pro Asn Ser Cys Ser Pro
1 5

<210> 50
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Codes for linker protein in GST-NANBV 15-17

<220>
<221> CDS
<222> (1)..(24)

<400> 50
ggg atc ccc aat tcc tgc agc cct
Gly Ile Pro Asn Ser Cys Ser Pro
1 5

24

<210> 51
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Carboxy-terminal linker protein in GST-NANBV 15-17

<400> 51

Gly Ile Gly Asn Ser Ser
1 5

<210> 52
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Codes for carboxy-terminal linker protein in GST-NANBV 15-17

<220>
<221> CDS
<222> (1)..(18)

<400> 52
ggg atc ggg aat tca tcg tga
Gly Ile Gly Asn Ser Ser
1 5

21

<210> 53
<211> 5
<212> PRT
<213> Artificial

<220>
 <223> Thrombin cleavage site in GST-NANBV 15-17

<400> 53

Val Pro Arg Gly Ser
 1 5

<210> 54
 <211> 15
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for thrombin cleavage site in GST-NANBV 15-17

<220>
 <221> CDS
 <222> (1)..(15)

<400> 54
 gtt ccg cgt gga tcc
 Val Pro Arg Gly Ser
 1 5

15

<210> 55
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Linker protein in GST-NANBV 15-17

<400> 55

Pro Ser Asn Ser Cys Ser Pro
 1 5

<210> 56
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for linker protein in GST-NANBV 15-17

<220>
 <221> CDS
 <222> (1)..(21)

<400> 56
 cca tcg aat tcc tgc agc cct
 Pro Ser Asn Ser Cys Ser Pro
 1 5

21

<210> 57

<211> 5
 <212> PRT
 <213> Artificial

<220>
 <223> Carboxy-terminal linker protein in GST-NANBV 15-17

<400> 57

Gly Ile His Arg Asp
 1 5

<210> 58
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 15-17

<220>
 <221> CDS
 <222> (1)..(15)

<400> 58
 gga att cat cgt gac tga
 Gly Ile His Arg Asp
 1 5

18

<210> 59
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> Linker protein in GST-NANBV 690-691

<400> 59

Gly Ile Pro Asn Ser Ser Ser Val Pro
 1 5

<210> 60
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for linker protein in GST-NANBV 690-691

<220>
 <221> CDS
 <222> (1)..(27)

<400> 60
 ggg atc ccc aat tcg agc tcg gta ccc
 Gly Ile Pro Asn Ser Ser Ser Val Pro
 1 5

27

<210> 61
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Carboxy-terminal linker protein in GST-NANBV 690-691

<400> 61

Thr Gly Ile Gly Asn Ser Ser
 1 5

<210> 62
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 690-691

<220>
 <221> CDS
 <222> (1)..(21)

<400> 62
 acg ggg atc ggg aat tca tcg tga 24
 Thr Gly Ile Gly Asn Ser Ser
 1 5

<210> 63
 <211> 66
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 63
 gatccatgag cacgattccc aaacctcaaa gaaaaaccaa acgtaacacc aaccgtcgcc 60
 cacagg 66

<210> 64
 <211> 66
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 64
 aattcctgtg ggggacggtt ggtgttacgt ttggtttttc tttgagggtt gggaatcgtg 60
 ctcattg 66

<210> 65
 <211> 759
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a fusion protein that includes sequences from
 glutathione-S-transferase, non-A, non-B hepatitis virus capsid
 antigen, and a thrombin cleavage site

<220>
 <221> CDS
 <222> (1)..(756)

<400> 65
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac 576
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

16988 ST25.txt

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc 624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt 672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

gga tcc atg agc acg att ccc aaa cct caa aga aaa acc aaa cgt aac 720
Gly Ser Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
225 230 235 240

acc aac cgt cgc cca cag gaa ttc atc gtg act gac tga 759
Thr Asn Arg Arg Pro Gln Glu Phe Ile Val Thr Asp
245 250

<210> 66
<211> 66
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 66
gatccgacgt caagttcgcg ggtggcggtc agatcggttg tggagtttac ttgttgccgc 60

gcaggg 66

<210> 67
<211> 66
<212> DNA
<213> Artificial

<220>
<223> synthetic oligonucleotide

<400> 67
aattccctgc gcggcaacaa gtaaactcca ccaacgatct gaccgccacc cggggaacttg 60

acgtcg 66

<210> 68
<211> 759
<212> DNA
<213> Artificial

<220>
<223> Codes for a fusion protein that includes sequences from
glutathione-S-transferase, non-A, non-B hepatitis virus capsid
antigen, and a thrombin cleavage site

<220>
<221> CDS
<222> (1)..(756)

<400> 68
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1	5	10	15		
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	20	25	30	96
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	35	40	45	144
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	50	55	60	192
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	65	70	75	240
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	85	90	95	288
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	100	105	110	336
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	115	120	125	384
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	130	135	140	432
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	145	150	155	480
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	528
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	672
gga tcc gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt	Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val	225	230	235	720
tac ttg ttg ccg cgc agg gaa ttc atc gtg act gac tga	Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp	245	250		759

<210> 69
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 69
 gaattcttac ctgcgcggca acaagtaaac tc

32

<210> 70
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic oligonucleotide

<400> 70
 gctggatcca gcacgattcc caaacctcaa ag

32

<210> 71
 <211> 816
 <212> DNA
 <213> Artificial

<220>
 <223> Codes for a fusion protein that includes sequences from
 glutathione-S-transferase, non-A, non-B hepatitis virus capsid
 antigen, and a thrombin cleavage site

<220>
 <221> CDS
 <222> (1)..(813)

<400> 71
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

16988 ST25.txt

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac 576
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc 624
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt 672
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 gga tcc agc acg att ccc aaa cct caa aga aaa acc aaa cgt aac acc 720
 Gly Ser Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
 225 230 235 240
 aac cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt cag atc gtt 768
 Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
 245 250 255
 ggt gga gtt tac ttg ttg ccg cgc agg gaa ttc atc gtg act gac tga 816
 Gly Gly Val Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
 260 265 270

<210> 72
 <211> 271
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 72

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

16988 ST25.txt

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

Gly Ser Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
225 230 235 240

Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
245 250 255

Gly Gly Val Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
260 265 270

<210> 73
<211> 326

16988 ST25.txt

<212> PRT

<213> non-A, non-B hepatitis virus

<400> 73

Met Ser Thr Ile Pro Lys Arg Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
 130 135 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr
 180 185 190

Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp Cys Pro
 195 200 205

Asn Ser Ser Val Val Tyr Glu Ala Ala Asp Ala Ile Leu His Thr Pro
 210 215 220

Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser Arg Cys Trp Val
 225 230 235 240

16988 ST25.txt

Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr
245 250 255

Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala Thr Leu Cys
260 265 270

Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Gly
275 280 285

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Asp Cys
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
305 310 315 320

Asp Met Met Met Asn Trp
325

<210> 74
<211> 315
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 74

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

16988 ST25.txt

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly
210 215 220

Arg Gly Ile Pro Asn Ser Ser Ser Val Pro Met Ser Thr Ile Pro Lys
225 230 235 240

Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val
245 250 255

Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro
260 265 270

Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu
275 280 285

Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
290 295 300

Pro Glu Gly Arg Thr Gly Ile Gly Asn Ser Ser
305 310 315

<210> 75
<211> 252
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 75

16988 ST25.txt

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

Gly Ser Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
225 230 235 240

Thr Asn Arg Arg Pro Gln Glu Phe Ile Val Thr Asp
245 250

<210> 76
 <211> 252
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 76

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

16988 ST25.txt

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val
 225 230 235 240

Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
 245 250